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C 4	425.6	16.5	226001	8	AF391808	AF391808 Zea mays
5	341.6	13.2	115787	8	AF466202	AF466202 Zea mays
6	331.4	12.8	7622	8	ZMPM82G	X58700 Zea mays ZM
C 7	328.4	12.7	95078	8	AF466931	AF466931 Zea mays
C 8	328.4	12.7	99156	8	AF466932	AF466932 Zea mays
9	311.4	12.1	346296	8	AF090447	AF090447 Zea mays
10	298.8	11.6	8227	8	AF167312	AF167312 Zea mays
11	295.4	11.4	130843	8	AF464738	AF464738 Zea mays
12	286.4	11.1	160480	8	AF123535	AF123535 Zea mays
C 13	285.4	11.1	1261	8	AF050452	AF050452 Zea mays
C 14	283.8	11.0	1259	8	AF050453	AF050453 Zea mays
15	281	10.9	3196	8	AF465642	AF465642 Zea mays
16	259.6	10.1	107835	8	AY078063	AY078063 Zea mays
C 17	258.2	10.0	106186	8	AF448416	AF448416 Zea mays
C 18	256.2	9.9	3892	8	AX099717	AX099717 Sequence
C 19	252.6	9.8	8987	8	ZMU6408	U6408 Zea mays re
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REFERENCE
1 (bases 1 to 2715)
AUTHORS
Crane, E. H., Rice, D. A., Simmons, C. R., Tossberg, J. T., Sandahl, G. A
and Zhang, L.

TITLE Maize mpri polynucleotides and methods of use
JOURNAL Patent: WO 0065037-A 5 02-NOV-2000;
PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES
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/organism="Zea mays"
/db_xref="taxon:4577"

Promoter 645 a 682 c 609 g 778 t 1 others
BASE COUNT 1.2715
ORIGIN

Query Match 100.0%; Score 2579.6; DB 6; Length 2715;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION Sequence 3 from Patent WO0065037.
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 VERSION AX041008.1 GI:11340604
 KEYWORDS
 SOURCE
 ORGANISM
 Zea mays.
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 7789)
 Crane, E.H., Rice, D.A., Simmons, C.R., Tossberg, J.T., Sandahl, G.A.
 and Zhang, L.
 Maize mpr1 polynucleotides and methods of use
 Patent: WO 0065037-A 3 02-NOV-2000;
 PIONEER HI-BRED INTERNATIONAL, INC. (US)
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3'UTR 5926..6124
 BASE COUNT 1975 a 1822 c 1824 g 2167 t 1 others
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 Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 3

AF050451/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

LTR

BASE COUNT

ORIGIN

Query Match 17.0%; Score 439; DB 8; Length 1231;
 Best Local Similarity 90.9%; Pred. No. 3e-106;
 Matches 497; Conservative 0; Mismatches 30; Indels 20; Gaps 2;

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 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1231)
 Samiuel, P.J., Gaut, B.S., Tikhonov, A., Nakajima, Y. and
 Bennetzen, J.L.
 The Paleontology of Intergene Retrotransposons of Maize: Dating the
 Strata
 Unpublished
 2 (bases 1 to 1231)
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 Direct Submission
 Submitted (23-FEB-1998) Biological Sciences, Purdue University,
 Hansen LSRB Rm 339, West Lafayette, IN 47907, USA
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 Matches 497; Conservative 0; Mismatches 49; Indels 12; Gaps 3;

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 Db 169707 CCGGACACTGTCGCGTGCACACCGGACAGTCCGCTGCGCTTCCGACCGTTGGCTGCG 169648
 QY 157 CACGTGTTGCGCGGATGCGCGCGGACACCGTGGCCCGGACCGGCTGCTACCGG 216
 Db 169647 CACGTGTTGCGCGGATGCGCGCGGACACCGTGGCCCGGACCGGCTGCTACCGG 169588
 QY 217 ACAGTCGCGTGACACACGACAGTCCGCTGAATTATAGCCGTACCGCTTAATCACTTCC 276
 Db 169587 ACAGTCGCGTGACACACGACAGTCCGCTGAATTATAGCCGTACCGCTTAATCTTCC 169528
 QY 277 CGAGACGACAGTTCGCTGACAGCTGACCGCTGCGGACCGGACACTGTCGCGTGAACCAAC 336
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 Db 169408 AATTGTTTCTGTTTCCAGACTTAGACCAATATAGTCTTAAACAAATGTA 169349
 QY 457 TTAATCTGAGAAACATACCTTTATACCTGTTGTAATTGTCACCA-----T 506
 Db 169348 TTAATCTGAGAAACATACCTTTATACCTGTTGTAATTGTCACCACTTTGATAG 169289
 QY 507 TTAACACTGGGCACTGTGTTGAGACCTAAATCAACAAATCTTAGAATGGCCCAAG 566
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RESULT 5
 AF466202
 LOCUS AF466202 115787 bp DNA linear PLN 12-MAR-2002

DEFINITION	Zea mays clone ZM88Bb.0138B04 putative aldose reductase-related protein, putative S-receptor kinase, putative genetic modifier, putative pp1ol, regulatory protein, putative SN protein, putative tnp2, putative gag protein, putative pol protein, putative pinhead protein, putative NADP-dependent malic enzyme, putative Foub gag/pol protein, and putative gag-pol precursor -orf2 genes, complete cds; and putative pol protein gene, partial cds.
ACCESSION	AF466202
VERSION	AF466202.1
KEYWORDS	GI:18542165
ORGANISM	Zea mays
SOURCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE	1 (bases 1 to 115787) Liaca,V., Linton,E., Young,S., Kovchok,S. and Messing,J.
AUTHORS	Direct Submission
TITLE	Submitted (07-JAN-2002) Rutgers, The State University of New Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute, 150 Frelinghuysen Road, Piscataway, NJ 08854, USA
JOURNAL	2 (bases 1 to 115787) Ramakrishna,W., Samiguel,P., Emberton,J. and Bennetzen,J.
REFERENCE	Direct Submission
AUTHORS	Submitted (07-JAN-2002) Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA
JOURNAL	Location/Qualifiers
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RESULT 6
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 ACCESSION X58700.1 GI:22447
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 KEYWORDS seed storage protein; zein protein.
 SOURCE Zea mays.
 ORGANISM Zea mays.
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 7622)
 Quayle,T.J.A.
 DIRECT SUBMISSION
 Submitted (21-SEP-1999) Quayle T.J.A., Institut fuer Biologie III,
 Universitaet Freiburg, Schenckstr.1, D-7800 Freiburg
 2 (bases 1 to 1715; 6320 to 7114)
 ANALYSIS Quayle,T.J., Brown,J.W. and Felix,G.
 Analysis of distal flanking regions of maize 19-kDa zein genes
 JOURNAL Gene 80 (2), 249-258 (1989)
 MEDLINE 90060774
 PUBMED 2583513
 COMMENT See X53582 for ZMPS1 gene.
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 Qy 458 TAATCTGAGAAACATACCTTTTACTGTTGTTTACTTTGTCACCC-----ATT 507
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 Qy 508 TAACACTTGGGCACTTGTGTGAGCACTTAATACCAAAATACTTGAATGCGCCACAG 567
 Db 49276 TCACATTGAAGCACTGTGTGTG-CACTCATCACCACCAAAATCTTGAATGCGCCACAG 49218
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RESULT 8
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DEFINITION Zea mays clone BAC 206C17, complete sequence.
ACCESSION AF466932
VERSION AF466932.1 GI:19908846
KEYWORDS
SOURCE Zea mays.
ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 99156)
 Ramakrishna, W., Emberton, J., Ogden, M., Sanmiguell, P. and
 Benneetzen, J.
TITLE Sequence and physical map analysis of the maize Rpi complex
 uncovers numerous modes and sites of local rearrangement
REFERENCE 2 (bases 1 to 99156)
AUTHORS Ramakrishna, W., Emberton, J., Ogden, M., Sanmiguell, P. and
 Benneetzen, J.
JOURNAL Direct Submission
RECORD Submitted (09-JAN-2002) Department of Biology, Purdue University,
 H334, Hansen Building, West Lafayette, IN 47907, USA
FEATURES Location/Qualifiers
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RESULT 10
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ACCESSION AF167312.1 GI:5825498
VERSION AF167312.1
KEYWORDS
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ORGANISM
Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 8227)
Christopher, M.E. and Good, A.G.
Evolution of a functionally related lactate dehydrogenase and
pyruvate decarboxylase pseudogene complex in maize
JOURNAL Genome 42 (6), 1167-1175 (1999)
MEDLINE 20123180
PUBMED 10659784
REFERENCE
2 (bases 1 to 8227)
Christopher, M.E. and Good, A.G.
Direct Submision
JOURNAL Submitted (08-JUL-1999) Biological Sciences, University of Alberta,
Edmonton, AB T6G 2E9, Canada
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RESULT 11
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LOCUS AF464738
DEFINITION Zea mays cultivar B73 putative gag protein, putative gag-pol
precursor, putative transposase, putative copia-type pol
polyprotein, putative copia-like retrotransposon Hopscotch
polyprotein, putative gag protein, putative prpol, putative prpol,
putative pol protein, putative pol protein, putative gag protein,
and teosinte branched protein genes, complete cds.
ACCESSION AF464738
VERSION AF464738.1 GI:18254408
KEYWORDS
SOURCE
ORGANISM
Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 130843)
Linton, E., Young, S., Kovchok, S., Keizer, G., Bronzino, A., Doebley, J.,
and Messing, J.
Direct Submision
JOURNAL Submitted (26-DEC-2001) Rutgers, The State University of New
Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute,

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REFERENCE
2 (bases 1 to 130843)
AUTHORS
Ramakrishna, M., SanMiguel, P., Emberton, J. and Bennetzen, J.
TITLE
Direct Substitution
JOURNAL
Submitted (26-DEC-2001) Department of Biological Sciences, Purdue
University, West Lafayette, IN 47907, USA

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Query Match 11.4%; Score 295.4; DB 8; Length 130843;
 Best Local Similarity 73.1%; Pred. No. 2e-67;
 Matches 410; Conservative 0; Mismatches 141; Indels 10; Gaps 2;

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RESULT 12
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 DEFINITION
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 ACCESSION
 AF123535
 VERSION
 AF123535.1 GI:7262818
 KEYWORDS
 Zea mays.
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
 clade; Panicoideae; Andropogoneae; Zea.
 SOURCE
 Zea mays.
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
 clade; Panicoideae; Andropogoneae; Zea.
 ORGANISM
 Zea mays.
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
 AUTHORS
 Tikhonov, A.P., Samiguel, P.J., Nakajima, Y., Gorenstein, N.M.,
 Bennetzen, J.L., and Avramova, Z.
 Colinearity and its exceptions in orthologous adh regions of maize
 and sorghum.
 Proc. Natl. Acad. Sci. U.S.A. 96 (13), 7409-7414 (1999)
 JOURNAL
 PUBMED
 10377428
 2 (bases 1 to 160480)
 REFERENCES
 Samiguel, P.J., Tikhonov, A. and Bennetzen, J.L.
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 Hansen USR, Rm. 339, West Lafayette, IN 47907, USA
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BASE COUNT 42638 a 37287 c 36880 g 43550 t 125 others
 ORIGIN

Query Match 11.1%; Score 286.4; DB 8; Length 160480;
 Best Local Similarity 75.7%; Pred. No. 5.4e-65;
 Matches 398; Conservative 0; Mismatches 116; Indels 12; Gaps 3;

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Db 69366 CCGTTGGCGCTTGGAGCGCGTGGCGGACAGTGTCCGTTGACACCGGACAGTCA 69424

QY 129 GGTGCGCCCTTCGACCGGTTGGCTCGGCGAGTGTTCGCGCGGATCGCGGACAGCG 188
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PS Claim 13; Page 85-86; 86bp; English.

CC The present invention provides the coding and protein sequences of the
CC maize NPR1 protein. NPR1 controls the onset of systemic acquired
CC resistance (SAR) in plants. SAR is the mechanism by which plants acquire
CC immunity to pathogens, and the sequences provided can be used to
CC produce transgenic plants with increased resistance to disease.

XX Sequence 2715 BP; 645 A; 682 C; 609 G; 778 T; 1 other;

Query Match 100.0%; Score 2579.6; DB 21; Length 2715;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 721 GACAGTCGATGATTAATAGCGGACGCGCTGTAATTCGCGAGTGGGCTGTTTGA 780
DB 721 GACAGTCGATGATTAATAGCGGACGCGCTGTAATTCGCGAGTGGGCTGTTTGA 780
QY 781 GGGGCGCTGGCTGTGACACCGAACAATGATGTCGCGCAAAATCAGACACTCAAGT 840
DB 781 GGGGCGCTGGCTGTGACACCGAACAATGATGTCGCGCAAAATCAGACACTCAAGT 840
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DB 961 GGTCAACTAATAATCTATTTATAGAAAGGTGTTAACCTTTTCCCTTTCAGCACT 1020
QY 1021 CTATATAGTCTTGAACCGGACATGAAGGTGTCTTAGAAGCCAGGCTCTCGGTTA 1080
DB 1021 CTATATAGTCTTGAACCGGACATGAAGGTGTCTTAGAAGCCAGGCTCTCGGTTA 1080
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DB 1141 GGTCTTAGATGATGATGACACTGTGGGTCTGTGCTTTTAAATTAAGTTATGATGA 1200
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DB 1621 TAACTTGTATGTAACAACTAATTTGAGAGGCTGATTTAGAGAAAGTCTGG 1680
QY 1681 GTGATATTAATGAGACGAATTCATGTTTAACTGTTGTGATTAATTAATTTCTAG 1740
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DB 1741 TTCAACGTCCTTGAAGGCGTGAAGAGTGTGAAATTTCCCTTCTTAATGATTTAAGA 1800
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DB 1801 GTAGAGTTTGTATCACTTATTAAGGATTCATTAAGGATTTATTTAGGATTAAGTTGA 1860
QY 1861 CATATTAATCTTCACTTCTTTTAAATAGTCAAGAAACCTTTCACACCTACTAGGA 1920
DB 1861 CATATTAATCTTCACTTCTTTTAAATAGTCAAGAAACCTTTCACACCTACTAGGA 1920
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DB 1921 GTACAGAAACATGACATATGATTTTGAAGAAAGATTTGACAGATTAAGTGT 1980

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D	901	TATGACCTGAGATTAATCAACTTACCAACTAGTTAGTCAATGGTTGTGTGAT	960
Q	961	CGCAACTCTAAATCTAATTTATGAAAGGTAAACCTATTTCCCTTACGACACT	1020
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D	1021	CTATATAGCTTGGAGACCTCGACATGAGGTGTCTTAGAGAACCAAGCTCGCGTAA	1080
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Q	1141	GGCTCAATATGCAATGACCTGACATGTCGCGTCGTCTCTTAATAAAGTATAGATGA	1200
D	1141	GGCTCAATATGCAATGACCTGACATGTCGCGTCGTCTCTTAATAAAGTATAGATGA	1200
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Q	1261	CTTTGCTTAAATAAAGATCCATATTTATATTTACTATGCAATATATATACCTCA	1320
D	1261	CTTTGCTTAAATAAAGATCCATATTTATATTTACTATGCAATATATATACCTCA	1320
Q	1321	CTATCTCGAAGATCATCTCGTGGGAGATAGAGTACTTTGAGAGTAAAGCTTTGA	1380
D	1321	CTATCTCGAAGATCATCTCGTGGGAGATAGAGTACTTTGAGAGTAAAGCTTTGA	1380
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Q	1561	TCAAATGACTGTTTTTTTGGACCTTTGACACATAGCCTTTAAAGTATTTCAATT	1620
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D	1621	TAAAGCTTTATGTAACAAACCTAATTTGAGAGGCGTATTTGAGAGAAAGTGTGG	1680
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D	1681	GTCGATGATCAATTTGACGAAATTCGATGTTAAACGTCTGTGATTTAAATTTCTAGC	1740
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Db	2101	GGTTTTCCCTCAAAATTGCGCGGAAATCTCGAATTTCTGGATTTTTTAATTGTTTAT	2160
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Db	2161	TCATATTCCTCCGCGGCGCTCTCTAGTCTATCTCTCTCCGTCGAGTGTGTCTTC	2220
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Db	2221	TTGCATCCACTTTTCCGCCCATCCCATCTCCCTACTTTCACGCAATCGTGTTCCGCC	2280
Oy	2281	GGACTCTTCTTCCACGATTCGTTGGACCCCTACCGCTCTCAGCAATCCTCCGCCCTC	2340
Db	2281	GGACTCTTCTTCCACGATTCGTTGGACCCCTACCGCTCTCAGCAATCCTCCGCCCTC	2340
Oy	2341	CCAGACACCGGCGAAACATCCCTCCACGTTATTCCTCGTAGACTATGTGCGCCCTTGG	2400
Db	2341	CCAGACACCGGCGAAACATCCCTCCACGTTATTCCTCGTAGACTATGTGCGCCCTTGG	2400
Oy	2401	TCCCTTTTCACTGTGTCTGAGATTTAGCCACCGCCCGGTAGAGAAAGGGAAGAC	2460
Db	2401	TCCCTTTTCACTGTGTCTGAGATTTAGCCACCGCCCGGTAGAGAAAGGGAAGAC	2460
Oy	2461	CATAATTTCTGTCTGTGCTGACGACGCGCGGTGAGATTTCACTCCGGATTGGCAAC	2520
Db	2461	CATAATTTCTGTCTGTGCTGACGACGCGCGGTGAGATTTCACTCCGGATTGGCAAC	2520
Oy	2521	GCTGGAGAGACTCGCGGTGATTTAGCCGCACTTCGCGCGCTCTAGAAAGGGTCAAGT	2580
Db	2521	GCTGGAGAGACTCGCGGTGATTTAGCCGCACTTCGCGCGCTCTAGAAAGGGTCAAGT	2580

```

RESULT 3
AAF81476
ID   AAF81476 standard; DNA, 3892 BP.
XX
XX   AAF81476;
AC
XX   08-JUN-2001 (first entry)
XX
XX   Corn promoter clone #700342976.
XX
XX   Corn; promoter; transgenic plant; herbicide resistance; ds.
XX
XX   Zea mays.
XX   OS
XX   WO200119976-A2.
XX
XX   22-MAR-2001.
XX
XX   13-SEP-2000; 2000MO-US25078.
XX   PF
XX   16-SEP-1999; 99US-0154182.
XX   PR
XX
XX   (MONS ) MONSANTO CO.
XX   PA
XX   Anderson HM, Chay CA, Chen G, Conner TW;
XX   PI
XX   WPI; 2001-244796/25.
XX   DR
XX
XX   Novel promoter nucleic acid sequences useful for regulating
XX   heterologous gene expression in plants, comprising regulatory sequences
XX   located upstream to plant DNA structural coding sequences -
XX   PT

```

XX Claim 1; Pages 99-100; 101pp; English.
 PS The present invention relates to novel corn promoter sequences (see
 CC AAF81456-AAF81478). The promoter sequences are useful for conferring
 CC expression of a second polynucleotide molecule in a transgenic plant
 CC tissue. In addition, the promoter sequences are useful for providing
 CC plants with herbicide resistance. The promoter sequences are suitable for
 CC selectively modulating expression of any operatively linked gene and
 CC provide additional regulatory element diversity in a plant expression
 CC vector in gene stacking approaches. The present sequence is one such corn
 CC promoter sequence isolated in the present invention.
 SO Sequence 3892 BP; 909 A; 1007 C; 877 G; 1099 T; 0 other;
 Query Match 9.9%; Score 256.2; DB 22; Length 3892;
 Best Local Similarity 71.3%; Pred. No. 6.3e-62;
 Matches 464; Conservative 0; Mismatches 98; Indels 89; Gaps 6;
 QY 20 CACTATGGGCGGAGAAATTTGGATCTCTCTTATTTGGCGAAGCCGTTGGCGCT 79
 DB 2088 CACCATACACTGCTCGGCTGCTGATGCTTCTTATCTGCGCGACCGCTTGAAGAT 2147
 QY 80 TTGGAGCCGTTGGCGGACCGGACACTGTCGCGTGCACACCGGACAGTGGCGCCCTT 139
 DB 2148 TTGGAGCCGTTGGCGGACCGGACACTGTCGCGCGACACCGGACAGTGGCGCCCTT 2207
 QY 140 CCGACCGTGGCTGCGGCGACGTTGTCGCGGATCGCGGCGGACCGTTGGCGCCGACC 199
 DB 2208 CAGACCGTGGCTGCGGCGTCAAGCGGATTCGCGGCGGACCGTTGGCGGACAGTC 2267
 QY 200 GACCGTGGCTGCGGCGGACCGGACACTGTCGCGTGCACACCGGACAGTGGCGCCCTT 258
 DB 2268 GACCGTGGCTGCGGCGGACCGGACACTGTCGCGTGCACACCGGACAGTGGCGCCCTT 2327
 QY 259 ACCGCGTGAATCACTTCCCGAGAGACGAAATTCGCGC-----TGAGCCAG 295
 DB 2328 ACACCGTGAATCACTTCCCGAGAGACGAAATTCGCGC-----TGAGCCAG 2387
 QY 296 -----TGAGCCAG 303
 DB 2388 GGTGATTTATAGCCATACACGCGTGCAGTCTGAGAGCGGATGTTCAACCGAGCTGCT 2447
 QY 304 CCGGCGGACCGGACACTGTCGCGTGCACACCGGACAGTGGCGCCCTTGAAGAT 363
 DB 2448 CCGGCGGACCGGACACTGTCGCGTGCACACCGGACAGTGGCGCCCTTGAAGAT 2507
 QY 364 TGACTTGGCTGGAACAAAGTCACTTTAGTTCCTTGAATTTTCTGTTTCCAGACT 423
 DB 2508 CTACCTTTGGCTGGAACAAAGTCACTTTTCCAAATTTGTTTCTGTTTCCAGACT 2567
 QY 424 TAGACACAATATACATTAGTCTTAAACAAATGTAATTTCTGAGAAACATACCTTTATAC 483
 DB 2568 TAGACACAATATACATTAGTCTTAAACAAATGTAATTTCTGAGAAACATACCTTTATAC 2625
 QY 484 TTGGTTTGAATTTGTCACCA-----TTTAACTTGGGCGACTTGGTTGGACA 533
 DB 2626 TTGATTCGACTTCATCCACCATTTGGCACTGTTTAACTTTAACTTTGGTTGG-CA 2684
 QY 534 CTAAATCACAATAATCTTAAATAGGCCCAAGGGGCACTTCCCTTCAA 584
 DB 2685 CTTAATCACAATAATCTTAAATAGGCCCAAGGGGCACTTCCCTTCAA 2735
 RESULT 4
 AAS96566 standard; DNA; 1587 BP.
 ID AAS96566;
 XX AAS96566;
 AC AAS96566;
 DT 26-FEB-2002 (first entry)
 XX Corn promoter sequence #9.
 DE

XX Corn; male reproductive tissue; plant regulatory sequence; Zea mays;
 KW Promoter; transcription regulation; operably linked gene; monocot;
 KW dicot; wheat anther; plant fertility; insect tolerance;
 KW pathogen tolerance; herbicide tolerance; ds.
 OS Zea mays.
 XX MO200183790-A2.
 XX 08-NOV-2001.
 XX 30-APR-2001; 2001WO-US13799.
 XX 01-MAY-2000; 2000US-201255P.
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 PA Conner TW, Dubois P, Malven M, Masucci JD;
 PI WPI; 2002-055481/07.
 DR Novel promoters isolated from corn for controlling gene expression in
 PT male reproductive tissues, such as anthers, tassels, and to regulate
 PT transcription of target genes including genes for insect or pathogen
 PT tolerance
 PS Claim 1; Page 111-112; 121pp; English.
 XX The present invention relates to the isolation of plant regulatory
 CC sequences from the male reproductive tissues of corn (Zea mays). The
 CC promoter sequences, fragments, regions or cis elements of the sequences,
 CC are capable of regulating transcription of an operably linked DNA
 CC sequence. The promoter sequences confer enhanced expression of operably
 CC linked genes in monocot or dicot male reproductive tissues, such as
 CC anthers, especially wheat anthers and is useful for regulating
 CC transcription of a DNA sequence, by operably linking the DNA sequence
 CC to the promoter. The promoter sequences are useful in plants to regulate
 CC transcription of target genes including genes for control of fertility,
 CC insect or pathogen tolerance and herbicide tolerance. They are also
 CC useful as probes or primers in nucleic acid hybridization experiments.
 CC The promoter sequences can be used in hybridization assays of other
 CC plant tissues to identify closely related or homologous genes and
 CC associated regulatory sequences. AAS96558-AAS96577 represent the
 CC corn promoter sequences of the present invention.
 SO Sequence 1587 BP; 435 A; 385 C; 375 G; 392 T; 0 other;
 Query Match 4.4%; Score 114.8; DB 24; Length 1587;
 Best Local Similarity 76.9%; Pred. No. 7.8e-22;
 Matches 140; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
 QY 41 GATCTCTTCTTATTTGGGAGAACCGGACCGTGGCGCTTGGAGCCGTTGGCGGACCGG 100
 DB 424 GATCTCTTCTTATTTGGGAGAACCGGACCGTGGCGCTTGGAGCCGTTGGCGGACCGG 483
 QY 101 AACTGTTCGGGTGCACACCGGACAGTCAAGTGGCCCTTCCAGCCGTTGGCTGCGGACAG 160
 DB 484 AACTGTTCGGGTGCACACCGGACAGTCAAGTGGCCCTTCCAGCCGTTGGCTGCGGACAG 543
 QY 161 TGTTCGCGGCGATCGCGGCGGACAGCCGTTGGGCCCGACCGAGCTTGCTACCGGACAG 220
 DB 544 TGTTCGCGGCGATCGCGGCGGACAGCCGTTGGGCCCGACCGAGCTTGCTACCGGACAG 603
 QY 221 TC 222
 DB 604 TC 605
 RESULT 5
 AAS14919/c
 ID AAS14919 standard; DNA; 3536 BP.
 XX

XX	AAS14919;
XX	27-FEB-2002 (first entry)
XX	DNA encoding maize glycine-rich promoter, ZmGRP.
XX	Maize; glycine-rich promoter; ZmGRP; transgenic plant; rye; rice;
KW	barley; sorghum; millet; sugar cane; tobacco; potato; soybean;
KW	insect resistance; herbicide resistance; stress resistance; mycotoxin;
KW	male sterility; ds.
XX	
OS	Zea mays.
XX	
PN	WO200170778-A2.
XX	
PD	27-SEP-2001.
XX	
PF	20-MAR-2001; 2001WO-US08965.
XX	
PR	21-MAR-2000; 2000US-0532806.
XX	
PA	(DEKA-) DEKALB GENETICS CORP.
XX	
PI	McElroy D, Orozco EM, Iaccetti LB,
XX	
DR	WPI; 2001-626124/72.
XX	
PT	An isolated nucleic acid comprising a maize glycine Rich protein
PT	promoter, useful for genetically engineering commercially important
PT	plants, e.g. maize, tomato and soybean -
XX	
PS	Claim 2, Fig 4; 185pp; English.

The invention relates to an isolated nucleic acid (I) comprising a maize Glycine Rich protein (GRP) promoter. (I) may be used in the production of transgenic monocotyledonous plants (wheat, maize (preferred), rye, rice, oat, barley, turf grass, sorghum, millet and/or sugar cane) or dicotyledonous plants (tobacco, tomato, potato, soybean (preferred), cotton, canola, alfalfa, sunflower and/or cotton) with altered properties such as insect/bacteria/fungi/viral/nematode/herbicide resistance, enhanced grain composition or quality/nutrient utilisation/eviroment or stress resistance, reduced mycotoxin contamination, male sterility, a selectable marker phenotype, a screenable marker phenotype, negative selectable marker phenotype or altered plant agronomic characteristics. The maize Glycine Rich Protein (GRP) promoter is a novel tool for the creation of transgenic plants (especially maize) with beneficial characteristics. The promoter minimises yield drag and other potential adverse physiological effects on maize growth and development that may be encountered by high-level, non-inducible, constitutive expression of a transgenic protein in a plant. A wider range of genetic promoters also makes it possible to introduce multiple transgenes into a plant, each of which is fused to a different promoter, therefore minimising the risk of DNA sequence homology dependent transgene inactivation (co-suppression). The present sequence represents the coding sequence of maize glycine rich promoter, ZmGRP as described in the invention.

Query Match	3.9%	Score 100.2	DB 23	Length 3536
Best Similarity	63.6%	Pred. No. 1,8e-17		
Matches 199	1	Mismatches 109	Indels 4	Gaps 3

Qy	706	TCGCGCGGTGACCGGACAGTCCCATGAATTATATGCGGAGCGGCGCTCGAATTTCCGAG	765
Db	1731	TCGGGGGACACTGACATTCGGTGATTTATGCGGAGCGGCGCTCAGAAACCCAA	1677
Qy	766	TGTGCGCTTTGAAGGAGGCGCTGCGCTGTGCAACGACATGTATGTGCGCCAAAA	825
Db	1671	GGTAAAGA-GTTGCAATATGATAGCGCCGTGGGCAACCGAACA--GTCCGGGCGCCGACACC	1615
Qy	826	TGAGCACTCAAGTCTTGTCTCATTTTATTATGTGTGCGTAACTGCAATTCCTTTTG	885

Dd	1614	AGAGTCTCTTCGGTTCCTTTTGGTCATTTCTTTTAAACCTTAAGTAAATTTTATGG	1555
Qy	886	GTTTGTGTGAACCTTATGCACTGAGTAATAATCACATTTAG-CCAACTAGTATAGTCCA	944
Dd	1554	GTTTGTGTGAACCTTATGCACTGAGTATATATATATTAAGGAAACCTGTATAGTCCA	1495
Qy	945	TGTGTGTTGTGTGATGTCGCAACTACTATAAATCTATTTATAGAAAGTGTAAACCCATTT	1004
Dd	1494	ATTATTTGTGTGTGACATTCACCAACCAAAATTTATTTATAGAAAAGGTAAACCCATTT	1435
Qy	1005	TCCCTTTACAGAC	1017
Dd	1434	TCCCTTTACAGTCT	1422

RESULT 6
AAS14920/c
ID AAS14920 standard; DNA; 8076 BP.

AC AAS14920;

DT 27-FEB-2002 (first entry)

DE Maize glycine-rich promoter, plasmid pZMGRP-GN73

KW Maize; glycine-rich promoter; ZmGRP; transgenic plant; rye; rice;

insect resistance; herbicide resistance; stress resistance; mycotoxin; KM

XX

Synthetic

PN WO200170778-A2.

PD 27-SEP-2001

20-MAR-2001; 2001WO-US089665.

21-MAR-2000; 2000US-0532806

AA
PA (DEKA-) DEKALB GENETICS CORP

AA
PI
MCELroy D, Orozco EM, Laccetti LB;

AA
DR
WPI: 2001-626124/72.

XX An isolated nucleic acid comprising a maize Glycine Rich Protein
PT

plants, e.g. maize, tomato and soybean - promoter, useful for genetically engineering commercially important

XX Example 2: Page 176-179: 185bp; English
PS

XX
XX The invention relates to an isolated nucleic acid (I) comprising a maize

CC Glycine Rich protein (GRP) promoter. (1) may be used in the production of
CC transgenic monocotyledonous plants (wheat, maize (preferred), rye, rice,
CC

CC oat, barley, turf grass, sorghum, millet and/or sugar cane) or
CC agricultural plants (tobacco, tomato, soybean (preferred),

CC cotton, canola, alfalfa, sunflower and/or cotton) with altered
CC cotton, canola, alfalfa, sunflower and/or cotton) with altered

resistance, enhanced grain composition or quality/nutrient

CC contamination, male sterility, a selectable marker phenotype, a selectable marker phenotype, negative selectable marker phenotype

CC or altered plant agronomic characteristics. The maize Glycine rich

CC plants (especially maize) with beneficial characteristics. The prom-

CC on maize growth and development that may be encountered by high-level

CC plant. A wider range of genetic promoters also makes it possible to

different promoter, therefore minimising the risk of DNA sequence


```

FT TATA_signal 2648..2654
FT /tag= a
FT /note= "pollen-specific"
FT complement (327..333)
FT
FT misc_signal
FT /tag= b
FT /standard_name= PB_core_motif
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen"
FT complement (550..556)
FT
FT misc_signal
FT /tag= c
FT /standard_name= PB_core_motif
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen"
FT
FT misc_signal
FT /tag= d
FT /standard_name= PB_core_motif
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen"
FT
FT misc_signal
FT /tag= e
FT /standard_name= LAT56/59_box
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen"
FT complement (1136..1142)
FT
FT misc_signal
FT /tag= f
FT /standard_name= PB_core_motif
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen;
FT nucleotide 1141 is shown as G in the
FT SEQ ID listing but is given as C in Fig.3"
FT complement (1140..1149)
FT
FT misc_signal
FT /tag= g
FT /standard_name= LAT56/59_box
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen"
FT
FT misc_signal
FT /tag= h
FT /standard_name= PB_core_motif
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen"
FT complement (1675..1681)
FT
FT misc_signal
FT /tag= i
FT /standard_name= LAT56/59_box
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen"
FT /tag= j
FT /standard_name= LAT56/59_box
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen"
FT complement (2213..2222)
FT
FT misc_signal
FT /tag= k
FT /standard_name= LAT56/59_box
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen"
FT complement (2315..2324)
FT
FT misc_signal
FT /tag= l
FT /standard_name= LAT56/59_box
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen"
FT complement (2370..2379)
FT
FT misc_signal
FT /tag= m
FT /standard_name= LAT56/59
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen"
FT complement (2669..2675)
FT
FT misc_signal
FT /tag= n
FT /standard_name= PB_core_motif
FT /note= "closely matches a cis-acting sequence
FT important for expression in pollen"
FT
FT misc_feature
FT /tag= o
FT /note= "ATG initiation codon"
FT /tag= p
FT /note= "ATG initiation codon"
FT /tag= p

```

FT	/note= "D17.12, Claim 3 (AAQ54890) "
FT	2527..2873
FT	promoter
FT	/*tag= "q"
FT	/note= "D17.2, Claim 3 (AAQ54891) "
FT	2497..2873
FT	promoter
FT	/*tag= "x"
FT	/note= "D18.5, Claim 3 (AAQ54892) "
FT	2410..2873
FT	promoter
FT	/*tag= "s"
FT	/note= "D16.6, Claim 3 (AAQ54893) "
FT	2279..2873
FT	promoter
FT	/*tag= "t"
FT	/note= "D16.4, Claim 3 (AAQ54894) "
FT	1295..2873
FT	promoter
FT	/*tag= "u"
FT	/note= "D10.2, Claim 3 (AAQ54895) "
FT	187..2873
FT	promoter
FT	/*tag= "v"
FT	/note= "p47.427, Claim 3 (AAQ54896) "
PN	WO9401572-A.
XX	
XX	20-JAN-1994.
XX	
PF	01-JUL-1993; 93WO-US06266.
XX	
PR	09-JUL-1992; 92US-0911532.
XX	
PA	(PION-) PIONEER HI-BRED INT INC.
PI	Allen RL, Lonsdale DM;
XX	
DR	WPI; 1994-035075/04.
XX	
PT	Maize pollen-specific polygalacturonase gene promoter - useful
PT	for conferring pollen-specificity on genes, e.g.
PT	beta-glucuronidase
XX	
PS	Claim 1; Fig 3; 69pp; English.
XX	
CC	The 2.87kb upstream sequence of maize polygalacturonase clone W247
CC	was isolated from a maize variety W22 genomic library. Analysis of
CC	the upstream region of known pollen-expressed genes from tomato
CC	revealed two cis-acting sequences important for expression in pollen.
CC	These were the PB core motif TGTGGT and the LAT56/59 box GAARTGTGA.
CC	In the maize PG gene upstream region there are 7 sequences with at
CC	least 5/7 matches to the PB core motif including the GTGC motif and
CC	6 sequences with at least 7/10 matches to the LAT56/59 box including
CC	the GTGA motif. The upstream region, or specific subfragments of it
CC	(see table p to v in the Features Table) can confer pollen-specific
CC	expression on genes fused downstream of it.
XX	
SQ	Sequence 2873 BP; 849 A; 546 C; 555 G; 923 T; 0 other;
Query Match	2.9%; Score 76; DB 15; Length 2873;
Best Local Similarity	61.4%; Pred. No. 1.3e-10;
Matches 172; Conservative	0; Mismatches 105; Indels 3; Gaps 3
Db	
QY	769 GGCGCTTTGAGAGGCCGCTGGCCTGGTCGACCGAACAATGTATGGGCGCAAAAATCA 828
DB	129 GTCCCTGGGACCCGACACACTGCTGGGGCATVACACAGCTCCGGTGCCAGATCAGS 188
QY	829 GCACACCTCAAGTCCCTTGGCTTCATTTTTATTTGTCGCTACTGATTTTCTTTGGTT 888
DB	189 GACCCCTTCGCTCTTTCCTTCCTTCCTTCCTTTTGAACCCTTAACCTTGATCGTTATTGGTT 248
QY	889 TGTGTTGAAC-TTATGACCTGAGATAATCACATCTAG-CGAAACTAGTTAGTCATG 946
DB	249 TGCTGTGAACCTTATGACACCTGTGGAATATATATATTAAGAACAACCTAGTGTCCAAT 308
QY	947 TGGTTTGGTGTGATGCTCACTACTAAATCTATTTATAGAAAGTGTAAACCTATTTC 1006
DB	309 CATTTGTGTGGCATTTAACCAACCAAATATATTATTARAGAAAAAGTTAAACCTTATTTC 368

Oy 1007 CCTTTC-AGCAGCTCTATATAGTCTTGAGACCTCGACA 1045
 Db 369 CCTTTCATCTCCCTTTTGGTATGATGCCAACACA 408

RESULT 9

AAQ54896
 ID AAQ54896 standard; DNA; 2687 BP.

AC AAQ54896;

XX 27-JAN-1995 (first entry)

DE Maize pollen-specific polygalacturonase gene promoter fragment.

KW Maize; pollen specific expression; polygalacturonase gene; promoter;
 KM Inbred corn variety W22; chimeric gene; ds.

XX Zea mays.

PN WO9401572-A.

PD 20-JAN-1994.

PF 01-JUL-1993; 93WO-US06266.

PR 09-JUL-1992; 92US-0911532.

PA (PION-) PIONEER HI-BRED INT INC.

PI Allen RL, Lonsdale DM;

DR WPI; 1994-035075/04.

PT Maize pollen-specific polygalacturonase gene promoter - useful
 PT for conferring pollen-specificity on genes, e.g.
 PT beta-glucuronidase

PS Claim 3; Page 41-42; 69pp; English.

XX The 2.87kb upstream sequence of maize polygalacturonase clone W2247
 CC (AAQ54896) was isolated from a maize variety W22 genomic library.
 CC Analysis of the upstream region of known pollen-expressed genes from
 CC tomato revealed two cis-acting sequences important for expression in
 CC pollen. These were the PB core motif TGTTGTT and the LAT56/59 box
 CC GAATTGGA. In the maize PG gene upstream region there are 7 sequences
 CC with at least 5/7 matches to the PB core motif including the GTGG
 CC motif and 6 sequences with at least 7/10 matches to the LAT56/59 box
 CC including the GTGA motif. The upstream region, or specific
 CC subregions of it, including AAQ54896, can confer pollen-specific
 CC expression on genes fused downstream of it.

SO Sequence 2687 BP; 811 A; 500 C; 495 G; 881 T; 0 other;

Query Match 2.5%; Score 64; DB 15; Length 2687;

Best Local Similarity 64.5%; Pred. No. 3.2e-07;

Matches 142; Conservative 0; Mismatches 75; Indels 3; Gaps 3;

Oy 829 GCAGACTCAAGCTCTTGGTATTTTATGTCGCTACTGATTTCTTTTGGTT 888

Db 3 GCACCTTCGGTTCCTTGGCTCTTGGCTTTGAACCTTAATTGATCGTTTATGTT 62

Oy 889 TGTGTTGAAC-TPANGACCTGAGATAAATCACTTACG-CAACTAGTTAGTCCATG 946

Db 63 TGTGTTGAACCTTTATGACCTGTGGAATATATTAATCTAGAACAACTAGTATGCTCAAT 122

Oy 947 TGTGTTGTTGATGCTCAACTACTAATAATCTATTTATAGAAAGGTAACTCCATTTT 1006

Db 123 CATTTGTGTGGGCAATCAACACCAAAATTTATTTATGAAAGGTAACTTATTTTC 1282

Oy 1007 CCTTTC-AGCAGCTCTATATAGTCTTGAGACCTCGACA 1045

Db 183 CCTTTCATCTCCCTTTTGGTATGATGCCAACACA 222

RESULT 10

AAQ78182/c
 ID AAQ78182 standard; DNA; 862 BP.

AC AAQ78182;

XX 02-JUN-1995 (first entry)

DE Maize associated region MAR1 (p2019227).

KW Genetic stabilising element; matrix associated region; MAR; ss.

XX Zea mays.

FN Key Location/Qualifiers

FT misc_feature 53..62

FT misc_feature 11..125

FT misc_feature 218..232

FT misc_feature 418..429

FT misc_feature 584..589

FT misc_feature 665..677

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

FT misc_feature 836..845

The term MAR refers to DNA segments isolated from nuclear scaffold or nuclear matrix preps. after endonuclease treatment. Two fragments, MAR1 (maize 0.8 kb AT rich region) and MAR2 (maize 1.25 kb regions with ARS3), found within a 5 kb maize EcoRI fragment have nuclear matrix binding activity. The sequence of the MAR1 fragment is given in AAQ78182 and that portion of MAR2 not previously sequenced is given in AAQ78183 along with the published portion of MAR2 named ARS3 (Berlanti et al. 1988 Plant Molecular Biology 11: 173-182). Additionally the sequence from the SAR1 (a region from a small heat shock gene (MAR3) (soybean HSP17.6 0.4 kb SAR1) is shown in AAQ78184 (Schoffl et al. Transgenic Res. 2 93-100 (1993)). MAR1,


```

FT      /*tag= ai
FT      /number= 12
FT      exon      12821..12931
FT      /*tag= aj
FT      /number= 13
FT      Intron    12932..13079
FT      /*tag= ak
FT      /number= 13
FT      exon      13080..13208
FT      /*tag= al
FT      /number= 14
FT      Intron    13209..16259
FT      /*tag= am
FT      /number= 14
FT      exon      16260..16363
FT      /*tag= an
FT      /number= 15
FT      Intron    16364..17235
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FT      exon      18130..18230
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FT      /number= 18
FT      Intron    18231..18458
FT      /*tag= au
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FT      exon      18457..18534
FT      /*tag= av
FT      /number= 19
FT      Intron    18535..18800
FT      /*tag= aw
FT      /number= 19
FT      exon      18801..18956
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FT      /number= 20
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FT      /*tag= ay
FT      /number= 20
FT      exon      19405..19479
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FT      /number= 21
FT      Intron    19480..19575
FT      /*tag= ba
FT      /number= 21
FT      exon      19576..19659
FT      /*tag= bb
FT      /number= 22
FT      Intron    19843..19849
FT      /*tag= bc
FT      misc_feature 23089..23101
FT      /*tag= bd
XX
XX      MO9964562-A2.
XX
XX      16-DEC-1999.
XX
XX      11-JUN-1999;
XX      99WO-US13266.
XX
XX      12-JUN-1998;
XX      98US-00890049.
XX      12-JUN-1998;
XX      98US-0089050.
XX

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PA      (UYBE-) UNIV PENNSYLVANIA STATE.
XX
XX      Guiltinan MJ, Kim K;
XX
XX      WPI, 2000-116538/10.
XX
XX      New gene regulatory sequences from plants used to provide resistance to
XX      microbial path pathogens -
XX

```

```

Query Match      2.0%; Score 52.8; DB 21; Length 23449;
Best Local Similarity 54.2%; Pred. No. 0.0018;
Matches 179; Conservative 1; Mismatches 133; Indels 17; Gaps 3;

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QY      717 ACCGACAGTCCGATGATTTAGCGGASCCGCGCTCGAATTTCCGAGTGCCTGTT 776
DB      23383 ACCGACAGTCCGATGATTTAGCGGASCCGCTCGAATTTCCGAGTGCCTGTT 23324
QY      777 TGAAAGCGCCCTGCGCTGTCACCGAACAATGATGTCGCCAATAACAGACACTC 836
DB      23323 CAGCGTGAAG-TCCCTGCTGTCACCGAACACTGGG-----CACACTTCGG 23280
QY      837 AAGTCCTTGTCTTCAATTTTATTTGTCGCTAAGTATTCCTTTGTTGTTGTTGA 896
DB      23279 TTATCCCTTGTCTTCTTTTGTGTAACCTAGTCTTGTCTTTTATTTGCTAAGTGA 23220
QY      897 ACCTTATGCACTGAGATTAATCACAATCTAGCCAACTAGTATGTCATGTGTTGTGT 956
DB      23219 CCTTTGGCACTGTATTAATCTTATACCTAGACAACTAGTATGTCATTAATTTGTGT 23160
QY      957 TGATCG-TCAACTACTATAAATCTATTTATAGAAAGTGTAAACCCATTTCCCTTGAC 1015
DB      23159 GGACAATTCACACCAACAAATCAATTAGAACCTAGTGAAGCTTAATTCCTTTCAATC 23100
QY      1016 ACACTTATATAGTCTTGACCTGCACA 1045
DB      23099 TCCCTTTTGTGATGATGCCAACACA 23070

```

RESULT 12

AAH88703 standard; DNA: 123219 BP.

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XX      AAH88703;
XX
XX      25-FEB-2002 (first entry)
XX
XX      Human DNA sequence SEQ ID 543.
XX
XX      Single nucleotide polymorphism; SNP; diallelic marker; human;
XX      central nervous system disorder; CNS; ds.
XX
XX      Homo sapiens.
XX
XX      WO200151659-A2.
XX
XX      19-JUL-2001.
XX
XX      11-JAN-2001; 2001WO-1B00116.
XX
XX      13-JAN-2000; 2000US-0175854.
XX
XX      (GEST ) GENSET.
XX
XX      Chu T, Blumenfeld M, Cohen D;
XX
XX      WPI, 2001-483085/52.
XX
XX      Isolated polynucleotides, useful for genotyping nucleic acids for
XX      diallelic markers for the diagnosis of depression, comprises central
XX      nervous system disorder related diallelic marker -
XX
XX      Disclosure; Page 439-472; 51pp; English.
XX

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XX Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation -
 PS Claim 1; SEQ ID NO 1163; 32pp + Sequence Listing; German.
 CC The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 XX

Seq Sequence 6215 BP; 1586 A; 169 C; 1366 G; 3094 T; 0 other;

Query Match 1.8%; Score 47.6; DB 24; Length 6215;
 Best Local Similarity 47.6%; Pred. No. 0.025;
 Matches 177; Conservative 0; Mismatches 189; Indels 6; Gaps 1;

QY 1524 TTGTCATTTATATATTTTCGTTCCATTAACAACCAAGTACTGTTTTTGA 1583
 DB 3889 TTATATATGATTTTATTTAGTATATATTTATTTTATTTATTTTGA 1583
 QY 1584 CCTTGACATAGCCTTAAAGTATTCACATTTAAGCTTTTANGTAAACAAAC 1643
 DB 3949 TATTTTATTTTATTTTATTTTAAATTTAAGTTGTTTATTTAGTATTT 4008
 QY 1644 TAAATTCAGAGAGGCTGATTTGAGAGAAAGTCGGGCTGATTCATTTGAGAA 1703
 DB 4009 TTTTGTATATTTGAGAGATTAATTAATTTATTTGATTTTATTTTATTT 4068
 QY 1704 TCGATGTTAACTGCTTGTATTAATTTCTAGCTTACACAGCTTGAACGGCTA 1763
 DB 4069 TAAATGAGTATTTATTTTATTTTAAATTTAAATTTTATTTTATTTAAG 4128
 QY 1764 GGAAGTGT-----TGGAATTTCCCTTCTATATGATTTATTAAGTGAAGTTTGTACAG 1817
 DB 4129 AGAAAAATGTTTATTAATAATGATATGATGAAAGTGTGTTTGTGCTTTTATGATAGA 4188
 QY 1818 TTATATTCAGATTTCAATTCGATTTATTTAGGATACGTTGACATTAAGTCTT 1877
 DB 4189 TTTGTTTATGTTTATTAATGATTTTGTGATATTTGTGAGATGAAGATGTTT 4248
 QY 1878 TCTTTTAAATA 1889
 DB 4249 TATTTTATTTA 4260

RESULT 15
 ABL54360
 ID ABL54360 standard; DNA; 5572 BP.

XX ABL54360;

XX 29-JUL-2002 (first entry)

DE Chemically treated apoptosis gene complementary to gene #30.

KW Apoptosis; HIV; Bloom syndrome; cardiopathy;
 KW neurodegenerative disorder; Herpes simplex virus; renal ischaemia;
 KW amyotrophic lateral sclerosis; cancer; ds.

OS Unidentified.

XX WO200177164-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-EP03969.

XX

PR 06-APR-2000; 2000DE-1019058.
 PR 07-APR-2000; 2000DE-1019173.
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A. Piepenbrock C. Berlin K.

XX WPI; 2002-017444/02.

PT Chemically modified sequences of genes associated with apoptosis are
 PT useful to determine methylation patterns of genomic DNA samples for
 PT diagnosis of associated diseases such as cancer -
 XX

PS Claim 1; Seq ID #60; 24pp; English.

CC This invention relates to chemically pre-treated DNA of genes
 CC associated with apoptosis. The nucleic acids are used to allocate
 CC patients for specific therapy for HIV infection, Bloom syndrome,
 CC cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus
 CC infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours
 CC and cancers. This nucleotide sequence represents a chemically
 CC treated apoptosis gene. Even SEQ ID numbers are the complementary
 CC DNA strands to the odd SEQ ID numbers. The sequence data for this
 CC patent is not represented in the printed specification but is based on
 CC information supplied by the European patent office.

Seq Sequence 5572 BP; 1307 A; 195 C; 1274 G; 2796 T; 0 other;

Query Match 1.8%; Score 47.4; DB 24; Length 5572;
 Best Local Similarity 46.3%; Pred. No. 0.027;
 Matches 156; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 1561 TCAAGTACTGTTTGTGACCTTGCACATAGCCTTAAAGTATTCACAT 1620
 DB 4630 TTAGATGCTTGCATTTTGAAGTTAGTATTTGCTTTTGAAGTGT 4689
 QY 1621 TAAGCTGTATGTAAACAACTAATTTGAGAGAGGCTGATTTGAGAGAAAGTCTGCG 1680
 DB 4690 TGGATTTATAGTGTGATTCATTTGTTTAAATTTGATTTTAAAGTGTGCTT 4749
 QY 1681 GTCATGATTCATTTGACGAAATGATTTTAACTGCTTGTGATTTAAATTTCTAGC 1740
 DB 4750 GTTGTGCTTATTTTGGGATTTATTTTAAATTTTGAATTTTGTGAGA 4809
 QY 1741 TTCACAGTCTTGAACGGCTGAGAGTGTGAATTTCCCTTCTATGATTTATTTAGA 1800
 DB 4810 TTTTGTGTTTGAATGATTTTATTTTGTGTTTATTTTATTTTATTTAGAGA 4869
 QY 1801 GTAGATTTTGTACAGTTTATTTTACGATTTTACGATTTTATTTAGGATACGTTGA 1860
 DB 4870 GTATATTTTATGATTTTATTTTGAAGATGATTTTATTTTATTTTGAAGATTTTGTATTTGG 4929
 QY 1861 CATATTAATTCAGTCTTTTATTTTAAATTTAGTCAAG 1897
 DB 4930 AAATGTTTAAATTTTATTTTATTTTATTTGATTTATAG 4966

Search completed: February 3, 2003, 16:20:48
 Job time : 727 secs

